

SEQUENCE LISTING

<110> Synaptic Pharmaceutical Corporation

<120> DNA Encoding A Human Melanin Concentrating Hormone Receptor (MCH1) And Uses Thereof

<130> 57453-A-PCT/JPW

<140> PCT/US99/31169

<141> 1999-12-30

<150> 09/224,426

<151> 1998-12-31

<160> 29

<170> PatentIn Ver. 2.1

<210> .1

<211> 1269

<212> DNA

<213> Homo sapiens

<400> 1

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ggtggcagggc gctggaggt gccgcagcct gcgtgggtgg aggggagctc agtcggttg 180  
tgggagcagg cgaccggcac tggctggatg gacctgaaag cctcgctgtc gcccaactgg 240  
cccaatgcca gcaacacactc tgatggcccc gataacctca ctccagcagg atcacctcct 300  
cgcacgggga gcatctcccta catcaacatc atcatgcctt cgtgttccgg caccatctgc 360  
ctccctggca tcatcgggaa ctccacggtc atcttcgggg tcgtgaagaa gtccaaagctg 420  
cactggtgca acaacgtccc cgacatcttc atcatcaacc tctcggtagt agatctcctc 480  
tttccctgg gcatgccctt catgatccac cagctcatgg gcaatgggggt gtggcacttt 540  
ggggagacca tgtgcacccct catcacggcc atggatgcca atagtcagtt caccagcacc 600  
tacatcctga ccgccatggc cattgaccgc tacctggca ctgtccaccc catcttcc 660  
acgaagttcc ggaagccctc tggccacc ctgggtatct gcctccctgtg ggccctctcc 720  
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cagttttcc tggccttgc cctgccttt gtggtcatca cagccgcata cgtgaggatc 900  
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aagagggtga cccgcacagc catcgccatc tgcgttgttct ttttgtgtc ctggccaccc 1020  
tactatgtgc tacagctgac ccagttgtcc atcagccgca cgaccctcac ctttgtctac 1080  
ttatacaatg cggccatcag cttgggctat gccaacagct gcctcaaccc ctttgtgtac 1140  
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ggcacctga 1269

<210> 2  
<211> 422  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15  
Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30  
Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45  
Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60  
Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80  
Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95  
Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met  
100 105 110  
Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser  
115 120 125  
Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn  
130 135 140  
Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu  
145 150 155 160  
Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly  
165 170 175  
Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp  
180 185 190  
Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile  
195 200 205  
Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg  
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser  
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe  
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr  
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu  
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met  
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr  
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val  
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser  
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu  
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys  
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln  
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
405 410 415

Thr Glu Ser Lys Gly Thr  
420

<210> 3  
<211> 1214  
<212> DNA  
<213> Rattus norvegicus

<400> 3  
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tgccagcaac atctccgatg gccaggataa tctcacattg ccggggtcac ctcctcgac 120  
agggagtgtc tcctacatca acatcattat gccttccgtg tttggtagca tctgtctcct 180  
gggcacatgtg ggaaactcca cggtcatctt tgctgtggtg aagaagtcca agctacactg 240  
gtgcagcaac gtccccgaca tcttcatcat caacctctct gtggtagatc tgctcttcct 300  
gctgggcatg ccttcatga tccaccagct catgggaac ggcgtctggc acttgggaa 360  
aaccatgtgc accctcatca cagccatgga cgccaaacagt cagttcacta gcacccat 420  
cctgactgcc atgaccattt accgctactt ggccaccgtc caccctatct cctccaccaa 480  
gttccggaag ccctccatgg ccaccctggt gatctgcctc ctgtggcgc tctccat 540  
cagtatcacc cctgtgtggc tctacgcccag gctcaitccc ttcccagggg gtgctgtggg 600  
ctgtggcatc cgccctgcca acccggacac tgacctctac tggttcaactc tgtaccagtt 660  
tttccctggcc tttgccttc cgttgtggt cattaccgccc gcatacgta aaataactaca 720  
gcgcacatgacg ttttcggtgg ccccagcctc ccaacgcagc atccggctc ggacaaagag 780  
ggtagccgc acggccattt ccacatgtct ggtcttctt gtgtgctggg caccctacta 840  
tgtgctgcag ctgaccacgc tgtccatcag cccggccacc ctcacgttg tctacttgc 900  
caacgcggcc atcagcttgg gctatgctaa cagctgcctg aaccctttt tgcatacatgt 960  
gctctgtgag accttcgaa aacgcttggt gttgtcagtg aagcctgcag cccagggca 1020  
gctccgcacg gtcagcaacg ctcagacacg tgcgtggag aggacagaaa gcaaggcac 1080  
ctgacaattc cccagtcgcc tccaagtca ggcacccat caaaccgtgg ggagagatac 1140  
tgagattaaa cccaggctt ccctgggaga atgcagaggc tggaggctgg gggctttag 1200  
caaccacatt ccac 1214

<210> 4  
<211> 353  
<212> PRT  
<213> Rattus norvegicus

<400> 4  
Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn  
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Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg  
20 25 30  
  
Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly  
35 40 45  
  
Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala  
50 55 60  
  
Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile  
65 70 75 80  
  
Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met  
85 90 95  
  
Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly  
100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe  
115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala  
130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala  
145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr  
165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val  
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe  
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile  
210 215 220

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala  
225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg  
245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr  
260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr  
275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser  
290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys  
305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gin Gly Gin Leu Arg Thr  
325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly  
340 345 350

Thr

<210> 5  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 5  
gggaactcca cggtcatctt cgcggt 26

<210> 6  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 6  
tagcggtaaa tggccatggc ggtcag 26

<210> 7  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 7  
ctcctggca tgcccttcataatccaccaggatcatggca atggg 45

<210> 8  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 8  
cttcttaggcc tgtacggaag tgtta 25

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 9  
gttgtggttt gtccaaactc atcaatg 27

<210> 10  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 10  
cgcgatcca ttatgtctgc actccgaagg aaatttg 37

<210> 11  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 11  
cgcgaattct tatgtgaagc gatcagagt cattttc 38

<210> 12  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 12  
gcggatccg ctatggctgg tgattctagg aatg 34

<210> 13  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 13  
ccggaaattcc cctcacacccg agccccctgg 29

<210> 14  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 14  
tcagctcggt tgtgggagca 20

<210> 15  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 15  
cttggacttc ttcacgac 18

<210> 16  
<211> 100  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 16

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu  
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Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95

Gly Ser Pro Pro  
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<210> 17  
<211> 100  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 17  
Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

85

90

95

Gly Ser Pro Pro  
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<210> 18  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 18  
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31

<210> 19  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 19  
cgaggcttcc aggtccgccc agccagtgcc g

31

<210> 20  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 20  
atgtcagtgg gagccgcgaa gaagggagtg gg

32

<210> 21  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 21  
cccaactccct tcttcgcggc tcccactgac at

32

<210> 22  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 22  
taatgtgtct aggtggcgtc agtgggagcc atg

33

<210> 23  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 23  
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33

<210> 24  
<400> 24  
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<210> 25  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 25  
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37

<210> 26

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer/probe

<400> 26  
gcccaggaga aagaggagat ctac

24

<210> 27  
<211> 422  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 27  
Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met  
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser  
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn  
130 135 140

Asn	Val	Pro	Asp	Ile	Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu
145					150						155			160	
Phe	Leu	Leu	Gly	Met	Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly
					165				170				175		
Val	Trp	His	Phe	Gly	Glu	Thr	Met	Cys	Thr	Leu	Ile	Thr	Ala	Met	Asp
					180				185				190		
Ala	Asn	Ser	Gln	Phe	Thr	Ser	Thr	Tyr	Ile	Leu	Thr	Ala	Met	Ala	Ile
					195				200				205		
Asp	Arg	Tyr	Leu	Ala	Thr	Val	His	Pro	Ile	Ser	Ser	Thr	Lys	Phe	Arg
					210			215				220			
Lys	Pro	Ser	Val	Ala	Thr	Leu	Val	Ile	Cys	Leu	Leu	Trp	Ala	Leu	Ser
					225			230			235		240		
Phe	Ile	Ser	Ile	Thr	Pro	Val	Trp	Leu	Tyr	Ala	Arg	Leu	Ile	Pro	Phe
					245			250				255			
Pro	Gly	Gly	Ala	Val	Gly	Cys	Gly	Ile	Arg	Leu	Pro	Asn	Pro	Asp	Thr
					260			265				270			
Asp	Leu	Tyr	Trp	Phe	Thr	Leu	Tyr	Gln	Phe	Phe	Leu	Ala	Phe	Ala	Leu
					275			280				285			
Pro	Phe	Val	Val	Ile	Thr	Ala	Ala	Tyr	Val	Arg	Ile	Leu	Gln	Arg	Met
					290			295			300				
Thr	Ser	Ser	Val	Ala	Pro	Ala	Ser	Gln	Arg	Ser	Ile	Arg	Leu	Arg	Thr
					305			310			315		320		
Lys	Arg	Val	Thr	Arg	Thr	Ala	Ile	Ala	Ile	Cys	Leu	Val	Phe	Phe	Val
					325			330				335			
Cys	Trp	Ala	Pro	Tyr	Tyr	Val	Leu	Gln	Leu	Thr	Gln	Leu	Ser	Ile	Ser
					340			345				350			
Arg	Pro	Thr	Leu	Thr	Phe	Val	Tyr	Leu	Tyr	Asn	Ala	Ala	Ile	Ser	Leu
					355			360				365			
Gly	Tyr	Ala	Asn	Ser	Cys	Leu	Asn	Pro	Phe	Val	Tyr	Ile	Val	Leu	Cys
					370			375			380				
Glu	Thr	Phe	Arg	Lys	Arg	Leu	Val	Leu	Ser	Val	Lys	Pro	Ala	Ala	Gln
					385			390			395		400		

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg  
405 410 415

Thr Glu Ser Lys Gly Thr  
420

<210> 28  
<211> 422  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 28  
Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu  
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp  
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Arg Arg Trp Arg Leu Pro  
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala  
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly  
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala  
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met  
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser  
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn  
130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu  
145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly

PROTEIN SEQUENCE

	165	170	175
Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp			
180	185	190	
Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile			
195	200	205	
Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg			
210	215	220	
Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser			
225	230	235	240
Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe			
245	250	255	
Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr			
260	265	270	
Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu			
275	280	285	
Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met			
290	295	300	
Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr			
305	310	315	320
Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val			
325	330	335	
Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser			
340	345	350	
Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu			
355	360	365	
Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys			
370	375	380	
Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln			
385	390	395	400
Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg			
405	410	415	
Thr Glu Ser Lys Gly Thr			

<210> 29  
<211> 353  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: mutated human  
MCH1

<400> 29  
Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn  
1 5 10 15  
  
Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg  
20 25 30  
  
Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly  
35 40 45  
  
Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala  
50 55 60  
  
Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile  
65 70 75 80  
  
Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met  
85 90 95  
  
Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly  
100 105 110  
  
Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe  
115 120 125  
  
Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala  
130 135 140  
  
Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala  
145 150 155 160  
  
Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr  
165 170 175  
  
Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val  
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe  
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile  
210 215 220

Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala  
225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg  
245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr  
260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr  
275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser  
290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys  
305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala  
325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly  
340 345 350

Thr